

1631

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/902,705

DATE: 10/15/2001

TIME: 13:51:23

Input Set : A:\PF138P1C1.ST25.txt

Output Set: N:\CRF3\10152001\I902705.raw

3 <110> APPLICANT: Bednarik et al.  
 5 <120> TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2  
 7 <130> FILE REFERENCE: PF138P1C1  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/902,705  
 C--> 9 <141> CURRENT FILING DATE: 2001-07-12  
 9 <150> PRIOR APPLICATION NUMBER: US 08/461,031  
 10 <151> PRIOR FILING DATE: 1995-06-05  
 12 <150> PRIOR APPLICATION NUMBER: PCT/US94/11914  
 13 <151> PRIOR FILING DATE: 1994-10-19  
 15 <160> NUMBER OF SEQ ID NOS: 11  
 17 <170> SOFTWARE: PatentIn version 3.1  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 1386  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Homo sapiens  
 24 <220> FEATURE:  
 25 <221> NAME/KEY: CDS  
 26 <222> LOCATION: (626)..(1264)  
 27 <223> OTHER INFORMATION:  
 30 <400> SEQUENCE: 1  
 31 gattttttgt gatattttct tcgggggggg ggggaacctt ttgtataaac gccaaccaac 60  
 33 cggccctttt ttgggtacct ggccatttta cttggcccat ttggtataaa tgttcctttc 120  
 35 cctgcgttaa tccccctgat tccttgtggg ataaccgcta tccccccct tagagtgaat 180  
 37 ttgaaaaccc ttgcgcccg aaggggaccg accgagccca gcgattcatg gagcgaggaa 240  
 39 agcggggaaga gcgcccaata cccaagccgc ctctcgcccg cgcgttgtgc gattcattaa 300  
 41 tacagctgcc gcgacaggtt tcccgactgg aaagcgggtc gtgagcgcaa cacaattaat 360  
 43 gtgagtttagc tcactcatta ggcacccag gctttacact ttatgcttcc ggctcgtatg 420  
 45 ttgtgtggaa ttgtgagcgg ataacaattt cacacaggaa acagctatga ccatgattac 480  
 47 gtccaagctc gaaattaacc ctactaaag ggaacaaaaa ctggagctcc accgcggtgg 540  
 49 cggcgcgtct agaactagt gatcccccg gctccaggaa ttccgccaga ccgggaggac 600  
 51 cgaggaggcg ccagactacg ggcga atg gcg acc cgc agc cct ggc gtc gtg 652  
 52 Met Ala Thr Arg Ser Pro Gly Val Val  
 53 1 5  
 55 att atg gat gat tgg cca ggg tat gac ttg aat tta ttc acg tac cca 700  
 56 ile Met Asp Asp Trp Pro Gly Tyr Asp Leu Asn Leu Phe Thr Tyr Pro  
 57 10 15 20 25  
 59 cag cac tat tat gga gac ttg gag tat gtc ctc atc cct cat ggt atc 748  
 60 Gln His Tyr Tyr Gly Asp Leu Glu Tyr Val Leu Ile Pro His Gly Ile  
 61 30 35 40  
 63 att gtg gac aga att gag cgg ctg gcc aag gat att atg aaa gac ata 796  
 64 ile Val Asp Arg ile Glu Arg Leu Ala Lys Asp ile Met Lys Asp ile  
 65 45 50 55  
 67 gga tat agt gac atc atg gtc ctg tgt gtg ctt aaa ggg ggg tac aaa 844  
 68 Gly Tyr Ser Asp ile Met Val Leu Cys Val Leu Lys Gly Gly Tyr Lys  
 69 60 65 70  
 71 ttc tgt gct gat ctc gta gaa cac ctt aag aac atc agc cga aat tca 892  
 72 Phe Cys Ala Asp Leu Val Glu His Leu Lys Asn ile Ser Arg Asn Ser

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73      75      80      85
75 gat cgg ttt gtc tca atg aag gtt gat ttc atc aga cta aaa agt tac      940
76 Asp Arg Phe Val Ser Met Lys Val Asp Phe Ile Arg Leu Lys Ser Tyr
77 90      95      100      105
79 agg aat gac cag tcc atg ggt gag atg cag ata atc gga ggc ggt gat      988
80 Arg Asn Asp Gln Ser Met Gly Glu Met Gln Ile Ile Gly Gly Gly Asp
81      110      115      120
83 ctt tca acg ctg gct gga aag aat ttt ctc att gtt gag gat gtt gtc      1036
84 Leu Ser Thr Leu Ala Gly Lys Asn Phe Leu Ile Val Glu Asp Val Val
85      125      130      135
87 gga act ggg agg acc atg aaa gca cta ctc agc aat ata gag aaa tac      1084
88 Gly Thr Gly Arg Thr Met Lys Ala Leu Leu Ser Asn Ile Glu Lys Tyr
89      140      145      150
91 aag ccc aac atg att aag gta gcc agt ttg ttg gtg aag aga aca tcc      1132
92 Lys Pro Asn Met Ile Lys Val Ala Ser Leu Leu Val Lys Arg Thr Ser
93      155      160      165
95 aga agt gac ggc ttt aga cct gac tat gct gga ttt gag att cca cac      1180
96 Arg Ser Asp Gly Phe Arg Pro Asp Tyr Ala Gly Phe Glu Ile Pro His
97 170      175      180      185
99 tta ttt gtg gtg gga tat gcc tta gat tac aat gaa tac ttc aga gat      1228
100 Leu Phe Val Val Gly Tyr Ala Leu Asp Tyr Asn Glu Tyr Phe Arg Asp
101      190      195      200
103 ctg aat cac ata tgc gtc atc aat gag cac ggg taa aggaaaatat      1274
104 Leu Asn His Ile Cys Val Ile Asn Glu His Gly
105      205      210
107 cgagtotttaa agacatgaat tctcaccact aaaggcccca gataggatca tttttacgcc      1334
109 tgtcttgggg agccagttgc aagttgggcc ccccgatc ttcacagga gg      1386
112 <210> SEQ ID NO: 2
113 <211> LENGTH: 212
114 <212> TYPE: PRT
115 <213> ORGANISM: Homo sapiens
117 <400> SEQUENCE: 2
119 Met Ala Thr Arg Ser Pro Gly Val Val Ile Met Asp Asp Trp Pro Gly
120 1      5      10      15
123 Tyr Asp Leu Asn Leu Phe Thr Tyr Pro Gln His Tyr Tyr Gly Asp Leu
124      20      25      30
127 Glu Tyr Val Leu Ile Pro His Gly Ile Ile Val Asp Arg Ile Glu Arg
128      35      40      45
131 Leu Ala Lys Asp Ile Met Lys Asp Ile Gly Tyr Ser Asp Ile Met Val
132      50      55      60
135 Leu Cys Val Leu Lys Gly Gly Tyr Lys Phe Cys Ala Asp Leu Val Glu
136 65      70      75      80
139 His Leu Lys Asn Ile Ser Arg Asn Ser Asp Arg Phe Val Ser Met Lys
140      85      90      95
143 Val Asp Phe Ile Arg Leu Lys Ser Tyr Arg Asn Asp Gln Ser Met Gly
144      100      105      110
147 Glu Met Gln Ile Ile Gly Gly Gly Asp Leu Ser Thr Leu Ala Gly Lys
148      115      120      125
151 Asn Phe Leu Ile Val Glu Asp Val Val Gly Thr Gly Arg Thr Met Lys

```

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Input Set : A:\PF138P1C1.ST25.txt

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152      130      135      140
155 Ala Leu Leu Ser Asn Ile Glu Lys Tyr Lys Pro Asn Met Ile Lys Val
156 145      150      155      160
159 Ala Ser Leu Leu Val Lys Arg Thr Ser Arg Ser Asp Gly Phe Arg Pro
160      165      170      175
163 Asp Tyr Ala Gly Phe Glu Ile Pro His Leu Phe Val Val Gly Tyr Ala
164      180      185      190
167 Leu Asp Tyr Asn Glu Tyr Phe Arg Asp Leu Asn His Ile Cys Val Ile
168      195      200      205
171 Asn Glu His Gly
172      210
175 <210> SEQ ID NO: 3
176 <211> LENGTH: 37
177 <212> TYPE: DNA
178 <213> ORGANISM: Artificial Sequence ✓
180 <220> FEATURE:
181 <223> OTHER INFORMATION: Primer for PCR ✓
183 <400> SEQUENCE: 3
184 tccgttatgg cgaccgcag cccctggcgtc gtgatta 37
187 <210> SEQ ID NO: 4
188 <211> LENGTH: 21
189 <212> TYPE: DNA
190 <213> ORGANISM: Artificial Sequence ✓
192 <220> FEATURE:
193 <223> OTHER INFORMATION: Primer for PCR ✓
195 <400> SEQUENCE: 4
196 catcaatgag cacgggtaaa g 21
199 <210> SEQ ID NO: 5
200 <211> LENGTH: 24
201 <212> TYPE: DNA
202 <213> ORGANISM: Artificial Sequence ✓
204 <220> FEATURE:
205 <223> OTHER INFORMATION: Primer for PCR ✓
207 <400> SEQUENCE: 5
208 gatcggagac tacgggcgaa tggc 24
211 <210> SEQ ID NO: 6
212 <211> LENGTH: 27
213 <212> TYPE: DNA
214 <213> ORGANISM: Artificial Sequence ✓
216 <220> FEATURE:
217 <223> OTHER INFORMATION: Primer for PCR ✓
219 <400> SEQUENCE: 6
220 caggtgcatac aatgagcacg ggtaaag 27
223 <210> SEQ ID NO: 7
224 <211> LENGTH: 218
225 <212> TYPE: PRT
226 <213> ORGANISM: Homo sapiens ✓
228 <400> SEQUENCE: 7
230 Met Ala Thr Arg Ser Pro Gly Val Val Ile Ser Asp Asp Glu Pro Gly

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Input Set : A:\PF138P1C1.ST25.txt

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231 1          5          10          15
234 Tyr Asp Leu Asp Leu Phe Cys Ile Pro Asn His Tyr Ala Glu Asp Leu
235          20          25          30
238 Glu Arg Val Phe Ile Pro His Gly Leu Ile Met Asp Arg Thr Glu Arg
239          35          40          45
242 Leu Ala Arg Asp Val Met Lys Glu Met Gly Gly His His Ile Val Ala
243          50          55          60
246 Leu Cys Val Leu Lys Gly Gly Tyr Lys Phe Phe Ala Asp Leu Leu Asp
247 65          70          75          80
250 Tyr Ile Lys Ala Leu Asn Arg Asn Ser Asp Arg Ser Ile Pro Met Thr
251          85          90          95
254 Val Asp Phe Ile Arg Leu Lys Ser Tyr Cys Asn Asp Gln Ser Thr Gly
255          100          105          110
258 Asp Ile Lys Val Ile Gly Gly Asp Asp Leu Ser Thr Leu Thr Gly Lys
259          115          120          125
262 Asn Val Leu Ile Val Glu Asp Ile Ile Asp Thr Gly Lys Thr Met Gln
263          130          135          140
266 Thr Leu Leu Ser Leu Val Arg Gln Tyr Asn Pro Lys Met Val Lys Val
267 145          150          155          160
270 Ala Ser Leu Leu Val Lys Arg Thr Pro Arg Ser Val Gly Tyr Lys Pro
271          165          170          175
274 Asp Phe Val Gly Phe Glu Ile Pro Asp Lys Phe Val Val Gly Tyr Ala
275          180          185          190
278 Leu Asp Tyr Asn Glu Tyr Phe Arg Asp Leu Asn His Val Cys Val Ile
279          195          200          205
282 Ser Glu Thr Gly Lys Ala Lys Tyr Lys Ala
283          210          215
286 <210> SEQ ID NO: 8
287 <211> LENGTH: 218
288 <212> TYPE: PRT
289 <213> ORGANISM: Cricetulus longicaudatus
291 <400> SEQUENCE: 8
293 Met Ala Thr Arg Ser Pro Ser Val Val Ile Ser Asp Asp Glu Pro Gly
294 1          5          10          15
297 Tyr Asp Leu Asp Leu Phe Cys Ile Pro Asn His Tyr Val Glu Asp Leu
298          20          25          30
301 Glu Lys Val Phe Ile Pro His Gly Val Ile Met Asp Arg Thr Glu Arg
302          35          40          45
305 Leu Ala Arg Asp Val Met Lys Glu Met Gly Gly His His Ile Val Ala
306          50          55          60
309 Leu Cys Val Leu Lys Gly Gly Tyr Lys Phe Phe Ala Asp Leu Leu Asp
310 65          70          75          80
313 Tyr Ile Lys Ala Leu Asn Arg Asn Ser Asp Arg Ser Ile Pro Met Thr
314          85          90          95
317 Val Asp Phe Ile Arg Leu Lys Ser Tyr Cys Asn Asp Gln Ser Thr Gly
318          100          105          110
321 Asp Ile Lys Val Ile Gly Gly Asp Asp Leu Ser Thr Leu Thr Gly Lys
322          115          120          125
325 Asn Val Leu Ile Val Glu Asp Ile Ile Asp Thr Gly Lys Thr Met Gln

```

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TIME: 13:51:23

Input Set : A:\PF138P1C1.ST25.txt

Output Set: N:\CRF3\10152001\I902705.raw

```

326      130      135      140
329 Thr Leu Leu Ser Leu Val Lys Arg Tyr Asn Pro Lys Met Val Lys Val
330 145      150      155      160
333 Ala Ser Leu Leu Val Lys Arg Thr Ser Arg Ser Val Gly Tyr Arg Pro
334      165      170      175
337 Asp Phe Val Gly Phe Glu Ile Pro Asp Lys Phe Val Val Gly Tyr Ala
338      180      185      190
341 Leu Asp Tyr Asn Glu Tyr Phe Arg Asp Leu Asn His Ile Cys Val Ile
342      195      200      205
345 Ser Glu Thr Gly Lys Ala Lys Tyr Lys Ala
346      210      215
349 <210> SEQ ID NO: 9
350 <211> LENGTH: 231
351 <212> TYPE: PRT
352 <213> ORGANISM: Plasmodium falciparum
354 <400> SEQUENCE: 9
356 Met Pro Ile Pro Asn Asn Pro Gly Ala Gly Glu Asn Ala Phe Asp Pro
357 1      5      10      15
360 Val Phe Val Lys Asp Asp Asp Gly Tyr Asp Leu Asp Ser Phe Met Ile
361      20      25      30
364 Pro Ala His Tyr Lys Lys Tyr Leu Thr Lys Val Leu Val Pro Asn Gly
365      35      40      45
368 Val Ile Lys Asn Arg Ile Glu Lys Leu Ala Tyr Asp Ile Lys Lys Val
369      50      55      60
372 Tyr Asn Asn Glu Glu Phe His Ile Leu Cys Leu Leu Lys Gly Ser Arg
373 65      70      75      80
376 Gly Phe Phe Thr Ala Leu Leu Lys His Leu Ser Arg Ile His Asn Tyr
377      85      90      95
380 Ser Ala Val Glu Met Ser Lys Pro Leu Phe Gly Glu His Tyr Val Arg
381      100      105      110
384 Val Lys Ser Tyr Cys Asn Asp Gln Ser Thr Gly Thr Leu Glu Ile Val
385      115      120      125
388 Ser Glu Asp Leu Ser Cys Leu Lys Gly Lys His Val Leu Ile Val Glu
389      130      135      140
392 Asp Ile Ile Asp Thr Gly Lys Thr Leu Val Lys Phe Cys Glu Tyr Leu
393 145      150      155      160
396 Lys Lys Phe Glu Ile Lys Thr Val Ala Ile Ala Cys Leu Phe Ile Lys
397      165      170      175
400 Arg Thr Pro Leu Trp Asn Gly Phe Lys Ala Asp Phe Val Gly Phe Ser
401      180      185      190
404 Ile Pro Asp His Phe Val Val Gly Tyr Ser Leu Asp Tyr Asn Glu Ile
405      195      200      205
408 Phe Arg Asp Leu Asp His Cys Cys Leu Val Asn Asp Glu Gly Lys Lys
409      210      215      220
412 Lys Tyr Lys Ala Thr Ser Leu
413 225      230
416 <210> SEQ ID NO: 10
417 <211> LENGTH: 210
418 <212> TYPE: PRT

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/902,705

DATE: 10/15/2001

TIME: 13:51:24

Input Set : A:\PF138P1C1.ST25.txt

Output Set: N:\CRF3\10152001\I902705.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date